From pathobiome to socio-pathosystems: questioning disease management practices in Corsica

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Keywords: Bacterial fixed variants; Bacterial genomics; Gene-ontology enrichment analysis

P27. Experimental evolution of a *Bacillus thuringiensis acrystalliferous* strain in *Galleria mellonella*.

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The continuous exposition of a pathogenic bacterium in a host during a serial passage experiment (SPE) may facilitate the apparition and posterior fixation of mutations that favour its growth and multiplication in the host environment1. These changes, can be traced during an SPE by whole genome sequencing of the evolved variants 2, 3. Here we describe the results obtained for a SPE using a *Bacillus thuringiensis* streptomycin resistant crystal minus strain (Bt407 Cry$^-$)4 using *Galleria mellonella* larvae as a host system. Our objective was to describe the history of the events, which arose during the evolution of the pathogen in one of its natural hosts and explain phenotypic variations based on genotypic differences. The parental strain was entirely re-sequenced by Illumina NextSeq system prior to the study in the host. An infection protocol was established where *G. mellonela* larvae were force-fed with spores of the Bt407 Cry$^-$ strain, and spores collected from dead larvae where used to re-infect new *G. mellonella* individuals in a next passage. The experiment lasted for 20 passages and with 9 lines in parallel. The genetic changes, which happened during the experimental evolution, were monitored by whole genome sequencing of the evolved populations at passages 5, 10, 15 and 20. In parallel, the SPE evolved strains were tested for virulence to *G. mellonella*, persistence (bacterial load in the cadavers) and resistance to antimicrobial peptides (lag times and growth rates in presence or absence of nisin, an antimicrobial peptide used as a food preservative) and compared with the initial parental bacteria and with populations evolved *in vitro*. The fitness of the evolved strains was also measured by mixing the same amount of the SPE evolved and ancestral lineages and measuring the outcome of competition by estimating the rate of change in their respective frequencies over the course of the competition trial.

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Keywords: Experimental evolution, gut ecosystem, whole genome sequencing, *Bacillus thuringiensis*

P28. From pathobiome to socio-pathosystems: questioning disease management practices in Corsica.

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Shifting from pathogen to pathobiome paradigm raises questions on infectious disease management strategies. Disease-based strategies can be antagonist to reach a level of animal health in animal farming systems. According to our results in Corsica, bovine tuberculosis, echinococcosis, trichinosis, hepatitis E virus and Aujeszky virus are pathogens found together in the same pig herds but these pathogens fall under various modes of regulations, based on the use of different tools.
For example, we show co-infection between Aujeszky and hepatitis E virus as an indicator of animal infectious interaction between domestic pigs and wild boars, which pattern is different according to herd management practices. Whereas Aujeszky virus is supposed to be the object of drastic management measures, HEV management does not exists. Else, whereas bovine tuberculosis and trichinosis are detected through systemic controls in slaughterhouses, bovine tuberculosis is subject to specific epidemiological surveys and prophylaxis on cattle but not on pigs. *Echinococcosis* and *trichinosis* raise questions on slaughterhouse geographical control at the scale of the territory, and the identification of various HEV strains highlight different infectious pathways.
Moreover, implementing a pathogen management measure can affect an equilibrium at the levels of the animal and the herds as well as at the level of the territory. The notion of socio-pathosystem provides a framework to capture multi-pathogen infection dynamics under various human management practices. This communication aims at presenting results from different studies carried out by INRA and its partners in Corsica, raising questions on how to implement relevant disease strategies that take into account complex microbial communities and the presence of diverse pathogens under diverse management devices within an animal territory.

P29. Development of MetaXplor: a viral metagenomics database.

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Recent metagenomics-based studies have identified hundreds of unknown viruses living in environmental and ornamental hosts. While genomic, transcriptomic and metagenomic next generation sequencing (NGS) datasets are exponentially increasing, a large part of the virus-related sequences is probably still missed because (i) bioinformatics tools are still under-developed and (ii) our scientific community does not always share datasets. It is therefore crucial to better share, clean, store and analyze these datasets in order to better describe and characterize the virus diversity. In order to fulfill this objective, we have developed a novel Web-accessible NoSQL database – called MetaXplor – that archives reads and contigs obtained from viral metagenomics studies. This database also displays modules of (i) geolocalization of the samples, (ii) searches using similarity-based method (BLAST approaches), (iii) searches using Keywords:, and (iv) phylogenetic placements of the reads on reference phylogenetic trees.

Keywords: Viral metagenomics, bioinformatic tools, database

P30. Air microbiota in animal slaughterhouse: how metagenomic detection can help epidemiological studies?